

K. Cannella • N

1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/436,184

DATE: 06/12/2000
TIME: 16:07:18

Input Set : A:\PT.txt
Output Set: N:\CRF3\06122000\I436184.raw

5 <110> APPLICANT: Wands, Jack R.
7 de la Monte, Suzanne M.
9 Ince, Nedim
11 Carlson, Rolf I.
15 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
19 <130> FILE REFERENCE: R.I. Hosp. - Malignant Neoplasms
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/436,184
25 <141> CURRENT FILING DATE: 1999-11-08
29 <160> NUMBER OF SEQ ID NOS: 7
33 <170> SOFTWARE: PatentIn Ver. 2.0
37 <210> SEQ ID NO: 1
39 <211> LENGTH: 36
41 <212> TYPE: PRT
43 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
49 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
51 EGF-like domain
55 <220> FEATURE:
57 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid
61 <400> SEQUENCE: 1
W--> 63 Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa
65 1 5 10 15
W--> 69 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa
71 20 25 30
W--> 75 Xaa Xaa Xaa Cys
77 35
82 <210> SEQ ID NO: 2
84 <211> LENGTH: 758
86 <212> TYPE: PRT
88 <213> ORGANISM: Homo sapiens
92 <400> SEQUENCE: 2
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96 1 5 10 15
100 Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
102 20 25 30
106 Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
108 35 40 45
112 Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
114 50 55 60
118 Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
120 65 70 75 80
124 Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
126 85 90 95
130 Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
132 100 105 110
136 Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
138 115 120 125

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142 Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
 144 130 135 140
 148 Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
 150 145 150 155 160
 154 Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
 156 165 170 175
 160 Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
 162 180 185 190
 166 Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
 168 195 200 205
 172 Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
 174 210 215 220
 178 Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
 180 225 230 235 240
 184 Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
 186 245 250 255
 190 Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
 192 260 265 270
 196 Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
 198 275 280 285
 202 Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
 204 290 295 300
 208 Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
 210 305 310 315 320
 214 Glu Gln Lys Ala Lys Val Lys Lys Lys Pro Lys Leu Leu Asn Lys
 216 325 330 335
 220 Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
 222 340 345 350
 226 Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val
 228 355 360 365
 232 Arg Lys Tyr Pro Gln Ser Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys
 234 370 375 380
 238 Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly
 240 385 390 395 400
 244 Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala
 246 405 410 415
 250 Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe
 252 420 425 430
 256 Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln
 258 435 440 445
 262 Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr
 264 450 455 460
 268 Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val
 270 465 470 475 480
 274 Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe
 276 485 490 495
 280 Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys
 282 500 505 510
 286 Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr

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288	515	520	525
292	Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr		
294	530	535	540
298	Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp		
300	545	550	555
304	Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp		
306	565	570	575
310	Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg		
312	580	585	590
316	Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala		
318	595	600	605
322	Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp		
324	610	615	620
328	Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala		
330	625	630	635
334	Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu		
336	645	650	655
340	Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro		
342	660	665	670
346	Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg		
348	675	680	685
352	Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys		
354	690	695	700
358	Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp		
360	705	710	715
364	Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu		
366	725	730	735
370	Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg		
372	740	745	750
376	Arg Ser Leu Pro Ala Ile		
378	755		
383	<210> SEQ ID NO: 3		
385	<211> LENGTH: 2324		
387	<212> TYPE: DNA		
389	<213> ORGANISM: Homo sapiens		
393	<400> SEQUENCE: 3		
395	cggaccgtgc aatggcccag cgtaaaatg ccaagagcag cggcaacacg agcagcagcg 60		
397	gctccggcag cggtagcacg aagtgcgggc gcagcagccc cggggccccc agagacaaac 120		
399	agcatggagg acacaagaatg ggaggaaaaag gcgactctc ggaaacttc ttcttcacgt 180		
401	ggtttatgtt gattgtatgg ctggcgctct ggacatctgtt agctgtcggtt tggtttgatc 240		
403	ttgttgacta tgaggaagtt cttagaaaaac taggaatcta tgatgtcgat ggtgtatggag 300		
405	atttgtatgtt ggatgtatgcc aaagttttat taggacttaa agagatct acttcagacg 360		
407	cagcgttccc gccagaaggat gctgagccac acactgtggcc acggaggcag gttccctgtgg 420		
409	aggcagaacc ccagaataatc gaagatggaaat caaaagaaca aattcgtatc cttctccatc 480		
411	aaatgttaca cgccagaacat gttgagggag aagacttgc acaagaagat ggaccacacg 540		
413	gagaaccaca acaagaggat gatgtatcc ttatggcgac tgatgtatgat gatagatgg 600		
415	agacccctggaa acctgtaaat tctcatggaa aaacccggacca tagttcacac gtggaaagaga 660		
417	cagtccatca acactgtatgg caggatgtgg aagagatgt gttcgacccatc gaaaatccatc 720		
419	attccactgtca accatgtatgtt gaaatgtttt gatgtatccatc tgatgtatgat gatgtatccatc 780		

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421 accaagtctta tgaggaacaa gcagtataatg aacctctaga aatgaaggg atagaatca 840
 423 cagaagtaac tgccccctt gaggataatc ctgtagaaga ttccacaggta attgtagaag 900
 425 aagaatcat ttttcctgtg gaagaacacgc aggaagtacc accagaaaca aatagaaaaa 960
 427 cagatgtcc agaacaaaaaa gcaaaaatgtt aaaaaaaaaa gcttaaactt ttaaataaat 1020
 429 ttgataagac tattaaatgtt gactttagtg ctgcagaaaa actccgtaa agggaaaaaa 1080
 431 ttgaggaagc agtgaatgca tttaaagaac tagtacgaa ataccctcg agtccacag 1140
 433 caagatatgg gaaggcgcag tggatggatg atttggctga gaagaggaga agtaatgagg 1200
 435 tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgtat gtccctgcag 1260
 437 acctgtgaa gctgatgtt aagcgtcgcg cagacaggca acaattctt ggtcatatga 1320
 439 gaggttccctt gtttaccctg cagagattag ttcaactatt tcccaatgtat acttccttaa 1380
 441 aaaaatgaccc tggcggtggg taccccttgc taggagataa tgacaatgca aagaaaagttt 1440
 443 atgaagaggt gctgatgtg acacctaattt atggcttgc taaaatgttccat tatggcttca 1500
 445 tcctgaaggc acagaacaaaatttgcgata gcatccatata tttaaaggaa ggaatagaat 1560
 447 ccggaaatcc tggcaactgtat gatgggatgttatttcca cctggggat gccatgcaga 1620
 449 gggttggaa caaagaggca tataagtgtt atgagcttgg gcacaagaga ggacactttg 1680
 451 catctgtctg gcaacgcgtca ctctacaatg tgaatggact gaaaagcacag ccttgggg 1740
 453 ccccaaaaaga aacgggtcac agacagttt taaaatgtttt agaaagaaac tggaaagttaa 1800
 455 tccgagatgaa aggcttgcgatgtggata aagccaaagg tctttctgt cctggggat 1860
 457 aaacacccatgg gggaaaaggag gactggggcc agttcacgtt gtggcggcaaa ggaagaagaa 1920
 459 atgaaatgtc ctgcaaaaggaa gctctaaaaa cctgtacccat actagaaaaag ttccccggaga 1980
 461 caacagatg cagaagaggg cagatcaatattccatcat gcaccccccggg actcacgtt 2040
 463 ggccgcacac agggcccaaa aactgcggc tccgaatgca cttggggctt gtgttccca 2100
 465 aggaaggctg caagattcga tggccaaacg agaccaggac ctggggggaa ggcaagggtgc 2160
 467 tcatcttgc tggatgttgg cttccggaaac tgacaccacaa gcagagacgc agccttccag 2220
 469 tattcatgtt ggtatgttgg cttccggaaac tgacaccacaa gcagagacgc agccttccag 2280
 471 caattttatgc tggatgttgg aactcttgg gaga 2324

474 <210> SEQ ID NO: 4

476 <211> LENGTH: 31

478 <212> TYPE: PRT

480 <213> ORGANISM: Artificial Sequence

484 <220> FEATURE:

486 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF-like

488 cysteine-rich repeat

492 <220> FEATURE:

494 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid

498 <400> SEQUENCE: 4

W > 500 Cys Asp Xaa Xaa Xaa Cys Xaa Xaa Lys Xaa Gly Asn Gly Xaa Cys Asp
 W > 502 1 5 10 15
 W > 506 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
 W > 508 20 25 30
 513 <210> SEQ ID NO: 5
 515 <211> LENGTH: 1242
 517 <212> TYPE: PRT
 519 <213> ORGANISM: Homo sapiens
 523 <400> SEQUENCE: 5
 525 Met Ala Ser Pro Pro Glu Ser Asp Gly Phe Ser Asp Val Arg Lys Val
 527 1 5 10 15
 531 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
 533 20 25 30

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537 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
539      35          40          45
543 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
545      50          55          60
549 Pro Leu Glu Ser Cys Phe Asn Ile Asn Lys Arg Ala Asp Ser Lys Asn
551  65          70          75          80
555 Lys His Leu Val Ala Leu Tyr Thr Arg Asp Glu His Phe Ala Ile Ala
557      85          90          95
561 Ala Asp Ser Glu Ala Glu Gln Asp Ser Trp Tyr Gln Ala Leu Leu Gln
563      100         105         110
567 Leu His Asn Arg Ala Lys Gly His His Asp Gly Ala Ala Ala Leu Gly
569      115         120         125
573 Ala Gly Gly Gly Gly Ser Cys Ser Gly Ser Ser Gly Leu Gly Glu
575      130         135         140
579 Ala Gly Glu Asp Leu Ser Tyr Gly Asp Val Pro Pro Gly Pro Ala Phe
581 145          150          155          160
585 Lys Glu Val Trp Gln Val Ile Leu Lys Pro Lys Gly Leu Gly Gln Thr
587      165         170         175
591 Lys Asn Leu Ile Gly Ile Tyr Arg Leu Cys Leu Thr Ser Lys Thr Ile
593      180         185         190
597 Ser Phe Val Lys Leu Asn Ser Glu Ala Ala Ala Val Val Leu Gln Leu
599      195         200         205
603 Met Asn Ile Arg Arg Cys Gly His Ser Glu Asn Phe Phe Phe Ile Glu
605      210         215         220
609 Val Gly Arg Ser Ala Val Thr Gly Pro Gly Glu Phe Trp Met Gln Val
611 225          230          235          240
615 Asp Asp Ser Val Val Ala Gln Asn Met His Glu Thr Ile Leu Glu Ala
617      245         250         255
621 Met Arg Ala Met Ser Asp Glu Phe Arg Pro Arg Ser Lys Ser Gln Ser
623      260         265         270
627 Ser Ser Asn Cys Ser Asn Pro Ile Ser Val Pro Leu Arg Arg His His
629      275         280         285
633 Leu Asn Asn Pro Pro Pro Ser Gln Val Gly Leu Thr Arg Arg Ser Arg
635      290         295         300
639 Thr Glu Ser Ile Thr Ala Thr Ser Pro Ala Ser Met Val Gly Gly Lys
641 305          310          315          320
645 Pro Gly Ser Phe Arg Val Arg Ala Ser Ser Asp Gly Glu Gly Thr Met
647      325         330         335
651 Ser Arg Pro Ala Ser Val Asp Gly Ser Pro Val Ser Pro Ser Thr Asn
653      340         345         350
657 Arg Thr His Ala His Arg His Arg Gly Ser Ala Arg Leu His Pro Pro
659      355         360         365
663 Leu Asn His Ser Arg Ser Ile Pro Met Pro Ala Ser Arg Cys Ser Pro
665      370         375         380
669 Ser Ala Thr Ser Pro Val Ser Leu Ser Ser Ser Ser Thr Ser Gly His
671 385          390          395          400
675 Gly Ser Thr Ser Asp Cys Leu Phe Pro Arg Arg Ser Ser Ala Ser Val
677      405         410         415
681 Ser Gly Ser Pro Ser Asp Gly Gly Phe Ile Ser Ser Asp Glu Tyr Gly

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/436,184

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Input Set : A:\PT.txt
Output Set: N:\CRF3\06122000\I436184.raw

L:23 M:270 C: Current Application Number differs, Replaced Current Application Number
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:69 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:69 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:75 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:75 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:500 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:500 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:500 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:506 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:506 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4